REMARKS

Applicants believe that the present application is now in condition for allowance. Favorable reconsideration of the application as amended is respectfully requested.

The Examiner is invited to contact the undersigned by telephone if it is felt that a telephone interview would advance the prosecution of the present application.

Respectfully submitted,

Date June 11, 2002

By _____

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Should additional fees be necessary in connection with the filing of this paper, or if a petition for extension of time is required for timely acceptance of same, the Commissioner is hereby authorized to charge Deposit Account No. 13-3402 for any such fees; and applicant(s) hereby petition for any needed extension of time.

MARKED UP VERSION ATTACHED TO AMENDMENT IN

SERIAL NO. 10/078,531

Marked up version of the paragraph starting at page , line to page , line is below:

Marked up version of the paragraph on page 3, lines 6-9, is below:

Figure 1 represents the DNA sequence **(SEQ ID NO: 1)** of BVH-P7 gene from serotype M1 S. pyogenes strain ATCC700294; SEQ ID NO: 1. The underlined portion of the sequence represents the region coding for the leader peptide.

Marked up version of the paragraph on page 3, lines 11-14, is below:

Figure 2 represents the amino acid sequence **(SEQ ID NO: 2)** BVH-P7 protein from serotype M1 S. pyogenes strain ATCC700294; SEQ ID NO: 2. The underline sequence represents the 21 amino acid residues leader peptide.

Marked up version of the paragraph on page 3, lines 16-22, is below:

Figure 3 depicts the comparison of the predicted amino acid sequences of the BVH-P7 open reading frames from Spy74 **(SEQ ID NO: 3)**, Spy70 **(SEQ ID NO: 4)**, Spy69 **(SEQ ID NO: 5)**, Spy68 **(SEQ ID NO: 6)**, Spy 60 **(SEQ ID NO: 7)**, ATCC12357 **(SEQ ID NO: 8)**, ATCC700294 **(SEQ ID NO: 2)** S. pyogenes strains by using the program Clustal W from MacVector sequence analysis software (version 6.5). Underneath the alignment, there is a consensus line where * and . characters indicate identical and similar amino acid residues, respectively.

Please delete the paragraph on page 27, Table 1, and replace it with the following paragraph:

Table 1. Oligonucleotide primers used for PCR amplifications of S. pyogenes BVH-P7 gene

Genes	Primers I.D. (SEQ ID NO)	Restriction site	Vector	Sequence
BVH-P7	DMAR293 (3)	*NdeI*	pET21b	5'GTAGTCACCCACCATATGGAAGTTTTTAG-3' **(SEQ ID NO: 9)**
BVH-P7	DMAR294 (4)	*NotI*	pET21b	5'TTTTTTCTTTGCGGCCGCAGTTATTAGT-3' **(SEQ ID NO: 10)**
BVH-P7	DMAR480a (5)	*BamHI*	pCMV-GH	5'-GGGGATCCCACCCACAATCAGG-3' **(SEQ ID NO: 11)**
BVH-P7	DMAR481a (6)	*SalI*	pCMV-GH	5'GGTTGTCGACAGTAAAGCAACGCTAGTG-3' **(SEQ ID NO: 12)**

Marked up version of the paragraph on page 27, lines 5-15, is below:

It was determined that the 3027-bp including a stop codon (TAA) open reading frame (ORF) of BVH-P7 encodes a 1008 amino-acid-residues polypeptide with a predicted pI of 6.18 and a predicted molecular mass of 111,494.44 Da. Analysis of the predicted amino acid residues sequence (SEQ ID NO :2) ~~using the PSORTII sofware~~ (Real World Computing Partnership (http://psort.nibb.ac.jp)) suggested the existence of a 21 ~~amino acid residues signal peptide~~ (MKKHLKTVALTLTTVSVVTHN) **(SEQ ID NO: 13)**, which ends with a cleavage site situated between an asparagine and a glutamine residues.

Analysis of the amino-acid-residues sequence revealed the presence of a cell wall anchoring motif (LPXTGX) **(SEQ ID NO: 14)** located bewteen residues 974 and 981.